



SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Klein, Theodore M.
Odell, Joan T.
Orozco, Emil M. Jr.

<120> PLANT CELL CYCLIN GENES

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<140> US/09/665,308

<141> 2000-09-19

<150> 60/078,735

<151> 1998-03-20

<150> PCT/US99/06047

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35 40 45
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Ile Glu Ala Val Gln Ala Asp Val Thr Ala His Met Arg Ser Ile Leu
50 55 60
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Lys	Cys	Pro	Ser	Leu	Thr	Ala	Ile	Arg	Asp	Lys	Tyr	Lys	Gln	His	Lys	
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 tctttgtcga aaaacaatac cccaacaaga ggcagcgggt tgtgttgggt gaacttccca 180
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 agatcancga atcttatgat tcggatatcc acgggtatct tcgtgaaatg gagatgcaga 360
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 20 25 30
 Gly Glu Leu Pro Asn Leu Gln Asn Leu Ile Val Ser Glu Thr Gln Asn
 35 40 45
 Xaa Arg Lys Glu Lys Xaa Leu Cys Xaa Lys Asn Pro Asn Glu Lys Lys
 50 55 60
 Pro Ser Pro Thr Asn Asn Asn Thr Phe Pro Ser Pro Gln Ile Xaa Glu
 65 70 75 80
 Ser Tyr Asp Ser Asp Ile His Gly Tyr Leu Arg Glu Met Glu Met Gln
 85 90 95
 Asn Lys Arg Arg Xaa Xaa Val Asp Thr Leu Lys Arg Leu Glu
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aaatatattg	aaagacagaa	actacaactt	cttggataaa	ctagcatgct	gattgcctca	420
aaatatgaag	agatctgtgc	gcctcgtggt	gaagaatttt	gtttcataac	tgataacaca	480
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 35 40 45
 Cys Ala Ser Tyr Ala Ala Glu Ile Tyr Arg Asn Leu Met Ala Ala Glu
 50 55 60
 Leu Ile Arg Arg Pro Lys Ser Asn Tyr Met Glu Thr Leu Gln Arg Asp
 65 70 75 80
 Ile Thr Lys Gly Met Arg Gly Ile Leu Ile Asp Trp Ala Leu Arg Phe
 85 90 95
 Leu Glu Glu Tyr Lys Leu Leu Pro Asp Thr Leu Tyr Leu Thr Val Tyr
 100 105 110
 Leu Ile Asp Gln Phe Leu Ser Arg Lys Tyr Ile Glu Arg Gln Lys Leu
 115 120 125
 Gln Leu Leu Gly Ile Thr Ser Met Leu Ile Ala Ser Lys Tyr Glu Glu
 130 135 140
 Ile Cys Ala Pro Arg Val Glu Glu Phe Cys Phe Ile Thr Asp Asn Thr
 145 150 155 160
 Tyr Thr Lys Asn Gln Val Leu Lys Met Glu Cys Glu Val Leu Asn Asp
 165 170 175
 Leu Gly Phe His Leu Ser Val Pro Thr Ile Lys Thr Phe Leu Arg Arg
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 Gly Tyr Leu
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 35 40 45
 Val Val Asp Gln Asp Glu Glu Tyr Val Ala Leu Leu Leu Ser Lys Glu
 50 55 60
 Ser Ala Ser Gly Gly Gly Gly Pro Val Glu Glu Met Glu Asp Trp Met
 65 70 75 80
 Lys Ala Ala Arg Ser Gly Cys Val Arg Trp Ile Ile Lys Thr Thr Ala
 85 90 95
 Met Phe Arg Phe Gly Gly Lys Thr Ala Tyr Val Ala Val Asn Tyr Leu

Leu Gln Leu Leu Ser Val Ala Cys Leu Ser Leu Ala Ala Lys Val Glu
 50 55 60
 Glu Arg Arg Pro Pro Arg Leu Pro Glu Phe Lys Leu Asp Met Tyr Asp
 65 70 75 80
 Cys Ala Ser Leu Met Arg Met Glu Leu Leu Val Leu Thr Thr Leu Lys
 85 90 95
 Trp Gln Met Ile Thr Glu Thr Pro Phe Ser Tyr Leu Asn Cys Phe Thr
 100 105 110
 Ala Lys Phe Arg His Asp Glu Arg Lys Ala Ile Val Leu Arg Ala Ile
 115 120 125
 Glu Cys Ile Phe Ala Ser Ile Lys Val Ile Ser Ser Val Gly Tyr Gln
 130 135 140
 Pro Ser Thr Ile Ala Leu Ala Ala Ile Leu Ile Ala Arg Asn Lys Glu
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 Gln Leu Met Met Leu
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35 40 45

Pro Pro Pro Pro Ser Pro Thr Thr Glu Asp Cys Tyr Ser Ile Ala Ser
50 55 60

Phe Ile Glu His Glu Arg Asn Phe Val Pro Gly Phe Glu Tyr Leu Ser
65 70 75 80

Arg Phe Gln Ser Arg Ser Leu Asp Ala Asn Ala Arg Glu Glu Ser Val
85 90 95

Gly Trp Ile Leu Lys Val His Ala Tyr Tyr Gly Phe Gln Pro Leu Thr
100 105 110

Ala Tyr Leu Ala Val Asn Tyr Met Asp Arg Phe Leu Asp Ser Arg Arg
115 120 125

Leu Pro Glu Thr Asn Gly Trp Pro Leu Gln Leu Val Ser Val Ala Cys
130 135 140

Leu Ser Leu Ala Ala Lys Met Glu Glu Pro Leu Val Pro Ser Leu Leu
145 150 155 160

Asp Leu Gln Ile Glu Gly Ala Lys Tyr Ile Phe Glu Pro Arg Thr Ile
165 170 175

Arg Arg Met Glu Leu Leu Val Leu Gly Val Leu Asp Trp Arg Leu Arg
180 185 190

Ser Val Thr Pro Leu Cys Phe Leu Ala Phe Phe Ala Cys Lys Val Asp
195 200 205

Ser Thr Gly Thr Phe Ile Arg Phe Leu Ile Ser Arg Ala Thr Glu Ile
210 215 220

Ile Val Ser Asn Ile Gln Glu Ala Ser Phe Leu Ala Tyr Trp Pro Ser
225 230 235 240

Cys Ile Ala Ala Ala Ala Ile Leu Thr Ala Ala Asn Glu Ile Pro Asn
245 250 255

Trp Ser Val Val Lys Pro Glu Asn Ala Glu Ser Trp Cys Glu Gly Leu
260 265 270

Arg Lys Glu Lys Val Ile Gly Cys Tyr Gln Leu Met Gln Glu Leu Val
275 280 285

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Ile	Asn	Asn	Asn	Gln	Arg	Lys	Leu	Pro	Leu	Leu	Lys	Val	Leu	Pro	Gln
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305					310					315					320
Phe	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Phe	Ser	Leu	Ser	Cys	Lys	Arg	Arg
				325					330					335	
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<400> 13

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gagaaaatta	taggggtgcta	ccaattaatg	caagaacttg	tgattgacaa	taaccagagg	780
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<210> 14
 <211> 318
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 <213> Glycine max

<400> 14

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Asp	Ser	Ser	Pro	Pro	Ser	Glu	Ala	Glu	Ser	Ile	Ala	Gly	Phe	Met	Glu
			20					25					30		

Asp	Glu	Arg	Asn	Phe	Val	Pro	Gly	Phe	Glu	Tyr	Leu	Asn	Arg	Phe	Gln
	35						40					45			
Ser	Arg	Ser	Leu	Asp	Ala	Ser	Ala	Arg	Glu	Glu	Ser	Val	Ala	Trp	Ile
	50					55					60				
Leu	Lys	Val	Gln	Ala	Tyr	Tyr	Ala	Phe	Gln	Pro	Val	Thr	Ala	Tyr	Leu
65					70					75					80
Ser	Val	Asn	Tyr	Leu	Asp	Arg	Phe	Leu	Asn	Ser	Arg	Pro	Leu	Pro	Pro
				85					90					95	
Lys	Thr	Asn	Gly	Trp	Pro	Leu	Gln	Leu	Leu	Ser	Val	Ala	Cys	Leu	Ser
			100					105					110		
Leu	Ala	Ala	Lys	Met	Glu	Glu	Ser	Leu	Val	Pro	Ser	Leu	Leu	Asp	Leu
		115					120					125			
Gln	Val	Glu	Gly	Ala	Lys	Tyr	Val	Phe	Glu	Pro	Lys	Thr	Ile	Arg	Arg
	130					135					140				
Met	Glu	Leu	Leu	Val	Leu	Gly	Val	Leu	Asp	Trp	Arg	Leu	Arg	Ser	Val
145					150					155					160
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Phe	Phe	Ala	Cys	Lys	Leu	Asp	Ser	Thr
				165					170					175	
Gly	Thr	Phe	Thr	Gly	Phe	Leu	Ile	Ser	Arg	Ala	Thr	Gln	Ile	Ile	Leu
			180					185					190		
Ser	Asn	Ile	Gln	Glu	Ala	Ser	Phe	Leu	Ala	Tyr	Trp	Pro	Ser	Cys	Ile
		195					200					205			
Ala	Ala	Ala	Ala	Ile	Leu	His	Ala	Ala	Asn	Glu	Ile	Pro	Asn	Trp	Ser
	210					215					220				
Leu	Val	Arg	Pro	Glu	His	Ala	Glu	Ser	Trp	Cys	Glu	Gly	Leu	Arg	Lys
225					230					235					240
Glu	Lys	Ile	Ile	Gly	Cys	Tyr	Gln	Leu	Met	Gln	Glu	Leu	Val	Ile	Asp
				245					250					255	
Asn	Asn	Gln	Arg	Lys	Pro	Pro	Lys	Val	Leu	Pro	Gln	Leu	Arg	Val	Thr
			260					265					270		
Ile	Ser	Arg	Pro	Ile	Met	Arg	Ser	Ser	Val	Ser	Ser	Phe	Leu	Ala	Ser
		275					280					285			
Ser	Ser	Ser	Pro	Ser	Ser	Ser	Ser	Leu	Ser	Cys	Arg	Arg	Arg	Lys	Leu
	290					295					300				
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 <211> 570
 <212> DNA
 <213> Triticum aestivum

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 <223> n = A, C, G or T

<220>
 <221> unsure

<222> (515)..(516)
 <223> n = A, C, G or T

 <220>
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 <223> n = A, C, G or T

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 gagatttggg ctccagaggt gaacgacttc atattgttct ccgacaacac atatactagg 180
 gagcagattc tgaggatgga gaaggcaatc ctgaacatgc ttgagtggaa cctgacagtg 240
 cccacacctt acgtcttcct cgtgtgattc gccaggccg catcctcctg agataagaag 300
 aacggcaagg aggtaaaagg aacaccagat tttaacaaat cctcagatgt agtacgtatc 360
 tccatttgcc aaacatgatc tattgctgaa ttctgttctc cctggtgtat tgtctaaatg 420
 gagacacgtc tttttttcgt ggactggcgc tctgtagtat ggacagaata tgtttgattc 480
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 <210> 16
 <211> 75
 <212> PRT
 <213> Triticum aestivum

 <220>
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 <222> (68)
 <223> Xaa = ANY AMINO ACID

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 Lys Tyr Glu Glu Ile Trp Ala Pro Glu Val Asn Asp Phe Ile Leu Phe
 20 25 30
 Ser Asp Asn Thr Tyr Thr Arg Glu Gln Ile Leu Arg Met Glu Lys Ala
 35 40 45
 Ile Leu Asn Met Leu Glu Trp Asn Leu Thr Val Pro Thr Pro Tyr Val
 50 55 60
 Phe Leu Val Xaa Phe Ala Lys Ala Ala Ser Ser
 65 70 75

 <210> 17
 <211> 1932
 <212> DNA
 <213> Zea mays

 <220>
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 <222> (8)
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 <222> (26)
 <223> n = A, C, G or T

 <220>
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 <222> (159)
 <223> n = A, C, G or T

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accagccacc cagcactcca gccgccagac cagagtctnc ggccgccg ccgcacgaca 180
ggagagggag agatacgcg gctttgactt gccgccggtg cggtccgtgcg tgcctggtgg 240
gaatagtggg agacgccggt acagtacagg agccatggcg ccgagctgct acgacgcggc 300
agcgtccatg ctctctcgcg ccgaggagca cagcagcatc ctgtggtacg aggaggagga 360
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cggcgcggaac ttgttcccgc cgcagtcgga ggaatgcgtg gccgggtctg tggagcggga 480
acgggaccac atgccggggc cgtgctacgg cgacaggctg cgcggcgggc gcggtgtgtc 540
ctgcgtccgc cgggaggccg tcgactggat ttggaaggct tacacgcacc acaggttccg 600
ccctctcact gcctacttgg cagtgaacta cctcgatcgc ttctctcgcg tgtctgaggt 660
gccggactgc aaggactgga tgacgcagct cctcgcggtg gcgtgcgttt ctctggcgcg 720
caagatggag gaaaccgccg tcccgcagtg cctggacctt caggaggctg gagacgcgcg 780
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tgcagccgcc gtggccggag acgtggacga cgcggacggc gtcgagaacg cctgctgcgc 1080
tcacgtagat aaggagcggg tgttgcggtg ccaggaagcg atcgggtcca tggcgctctc 1140
ggcggccatt gacgacgcta ccgtgccacc gaaatctgcg agacgcagga gctcccccg 1200
gcccggtgccg cagagccctg tgggggtgct ggacgcggct ccctgcctca gctacaggag 1260
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aaaaaaaaaa ac 1932

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<210> 18
<211> 388
<212> PRT
<213> Zea mays

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<400> 18
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Glu Glu His Ser Ser Ile Leu Trp Tyr Glu Glu Glu Glu Glu Glu Leu
20 25 30

Glu Ala Val Gly Arg Arg Ser Gly Arg Ser Pro Gly Tyr Gly Asp Asp
35 40 45

Phe Gly Ala Asp Leu Phe Pro Pro Gln Ser Glu Glu Cys Val Ala Gly
50 55 60

Leu Val Glu Arg Glu Arg Asp His Met Pro Gly Pro Cys Tyr Gly Asp
65 70 75 80

Arg Leu Arg Gly Gly Gly Gly Cys Leu Cys Val Arg Arg Glu Ala Val
85 90 95

Asp Trp Ile Trp Lys Ala Tyr Thr His His Arg Phe Arg Pro Leu Thr
100 105 110

Ala Tyr Leu Ala Val Asn Tyr Leu Asp Arg Phe Leu Ser Leu Ser Glu
115 120 125

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Val	Pro	Asp	Cys	Lys	Asp	Trp	Met	Thr	Gln	Leu	Leu	Ala	Val	Ala	Cys
130						135					140				
Val	Ser	Leu	Ala	Ala	Lys	Met	Glu	Glu	Thr	Ala	Val	Pro	Gln	Cys	Leu
145					150					155					160
Asp	Leu	Gln	Glu	Val	Gly	Asp	Ala	Arg	Tyr	Val	Phe	Glu	Ala	Lys	Thr
				165					170					175	
Val	Gln	Arg	Met	Glu	Leu	Leu	Val	Leu	Thr	Thr	Leu	Asn	Trp	Arg	Met
			180					185					190		
His	Ala	Val	Thr	Pro	Phe	Ser	Tyr	Val	Asp	Tyr	Phe	Leu	Asn	Lys	Leu
		195					200					205			
Asn	Asn	Gly	Gly	Ser	Thr	Ala	Pro	Arg	Ser	Cys	Trp	Leu	Leu	Gln	Ser
	210					215					220				
Ala	Glu	Leu	Ile	Leu	Arg	Ala	Ala	Arg	Gly	Thr	Gly	Cys	Val	Gly	Phe
225					230					235					240
Arg	Pro	Ser	Glu	Ile	Ala	Ala	Ala	Val	Ala	Ala	Ala	Val	Ala	Gly	Asp
				245					250					255	
Val	Asp	Asp	Ala	Asp	Gly	Val	Glu	Asn	Ala	Cys	Cys	Ala	His	Val	Asp
			260					265					270		
Lys	Glu	Arg	Val	Leu	Arg	Cys	Gln	Glu	Ala	Ile	Gly	Ser	Met	Ala	Ser
		275					280					285			
Ser	Ala	Ala	Ile	Asp	Asp	Ala	Thr	Val	Pro	Pro	Lys	Ser	Ala	Arg	Arg
	290					295					300				
Arg	Ser	Ser	Pro	Val	Pro	Val	Pro	Gln	Ser	Pro	Val	Gly	Val	Leu	Asp
305					310					315					320
Ala	Ala	Pro	Cys	Leu	Ser	Tyr	Arg	Ser	Glu	Glu	Ala	Ala	Thr	Ala	Thr
				325					330					335	
Ala	Thr	Ala	Thr	Ser	Ala	Ala	Ser	His	Gly	Ala	Pro	Gly	Ser	Ser	Ser
			340					345					350		
Ser	Ser	Ser	Thr	Ser	Pro	Val	Thr	Ser	Lys	Arg	Arg	Lys	Leu	Ala	Ser
		355					360					365			
Arg	Cys	Asp	Gly	Ser	Cys	Ser	Asp	Arg	Ser	Lys	Arg	Ala	Pro	Ala	Gln
	370					375					380				
Trp	Thr	Lys	Glu												
385															

<210> 19
 <211> 481
 <212> DNA
 <213> Oryza sativa

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 <222> (88)
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tctccgccgn cgacatccag aggggcgagg agttcatgtt cgacgaggcg aaaatccagc 180
gcatggagca gatggtgctc aacgcgctgg agtggcggac gcgctccgtc acgcccgtcg 240
ccttcctcgg nttctttctc tccgcgtggt tcccgcgaagc cgcggcaccc ggcgctgctc 300
gatgccatca nggcccgcgc gtcgagctcc tcctccgcgt ctaagccggg angtgaacna 360
tggtgggagt tctccccctt cggtggccgg ccgncgcggn tctcctcncn gccgncggan 420
aaggcntccg gnngcccaaa ctccttcnct tccaaanctg nnggccccgn tttgncccct 480
t 481

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<210>  20
<211>  110
<212>  PRT
<213>  Oryza sativa

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<220>
<221>  UNSURE
<222>  (26)
<223>  Xaa = ANY AMINO ACID

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<220>
<221>  UNSURE
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<223>  Xaa = ANY AMINO ACID

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<220>
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Pro Arg Leu Leu Ala Ile Ser Cys Leu Xaa Leu Ala Ala Lys Met Gln
          20          25          30

Arg Ala Ala Ala Ile Ser Ala Xaa Asp Ile Gln Arg Gly Glu Glu Phe
          35          40          45

Met Phe Asp Glu Ala Lys Ile Gln Arg Met Glu Gln Met Val Leu Asn
          50          55          60

Ala Leu Glu Trp Arg Thr Arg Ser Val Thr Pro Leu Ala Phe Leu Gly
65          70          75          80

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Phe Phe Leu Ser Ala Trp Phe Pro Gln Ala Ala Ala Pro Gly Ala Ala
85 90 95

Arg Cys His Xaa Gly Arg Ala Val Glu Leu Leu Leu Arg Val
100 105 110

<210> 21
<211> 789
<212> DNA
<213> Triticum aestivum

<400> 21
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ctcaccgcct cgaccaaaat gtgatttgag gcaaattctg cgtttgaggc aaggacaata 120
aaagtgatgg agctttttggt cttcagcacc ttgaaatgga ggatgcaagc tggtactgct 180
tgctcgttta ttgactactt ccttttgcaa ttcaatgatc atgacacacc ctccatgctt 240
gcattctcct gctcaactga cctcatcctg agcacaacta agtgagctga ttttttggtg 300
ttcagacatt cagagattgc tggaagtgtt gcacttcctt catttgggga gcacaagact 360
tcagttgtcg aaatggctac aactaattgc aagtatataa acaagggagt gtgatgtgac 420
aggaaagatc ctgatgaagt gcttccttta tggaatgcct atctgaagtt tggactaaga 480
gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag 540
atgtttttat tgtagattag gatatgtgtg ttctgccacc ggttcgactt ctcattattag 600
aaggcaagca gttagtcat atcttactac tttgcactat tgtagatgga tgggtgaggga 660
ttgagaggct actactatta atgtgcgtaa actttgcac tttagctctc taaatgaaac 720
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aaaaaaaaa 789

<210> 22
<211> 163
<212> PRT
<213> Triticum aestivum

<220>
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<222> (28)
<223> Xaa = ANY AMINO ACID

<220>
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<222> (95)
<223> Xaa = ANY AMINO ACID

<220>
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<222> (138)
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Pro Ser Ser Asp Leu Thr Ala Ser Thr Lys Met Xaa Phe Glu Ala Asn
20 25 30

Ser Ala Phe Glu Ala Arg Thr Ile Lys Val Met Glu Leu Leu Val Phe
35 40 45

Ser Thr Leu Lys Trp Arg Met Gln Ala Val Thr Ala Cys Ser Phe Ile
50 55 60

Asp Tyr Phe Leu Cys Lys Phe Asn Asp His Asp Thr Pro Ser Met Leu
65 70 75 80

Ala Phe Ser Cys Ser Thr Asp Leu Ile Leu Ser Thr Thr Lys Xaa Ala

85										90					95									
Asp	Phe	Leu	Val	Phe	Arg	His	Ser	Glu	Ile	Ala	Gly	Ser	Val	Ala	Leu									
100										105					110									
Pro	Ser	Phe	Gly	Glu	His	Lys	Thr	Ser	Val	Val	Glu	Met	Ala	Thr	Thr									
115										120					125									
Asn	Cys	Lys	Tyr	Ile	Asn	Lys	Gly	Val	Xaa	Cys	Asp	Arg	Lys	Asp	Pro									
130										135					140									
Asp	Glu	Val	Leu	Pro	Leu	Trp	Asn	Ala	Tyr	Leu	Lys	Phe	Gly	Leu	Arg									
145										150					155					160				

Asp Met Leu

<210> 23
 <211> 1132
 <212> DNA
 <213> Zea mays

<220>
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 <222> (441)
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 gcgcgctccg gctcggcgac cagccctgga tggcgcgccct agccgccgct acctgcttcg 180
 cgctcgcgcg caaggtcgag gagacgcgcg tgccgccgct cctcgacctc cagctctacg 240
 ccgccgctga cgccgcggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc 300
 tgctcgtgct ctccgcgctt ggggtggcgga tgcacctgt cagcccttc tcctacctcc 360
 agcccgtcct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgct ctgctcgcgg 420
 tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggcccgc gccgcgttgc 480
 tgatcacagc cgccgccggc gacggcggcg acggcgacgg cgacacggag ctccctggcg 540
 tcatcaatgc ccccgaggac aagaccgccg agtgtgccaa gatcatctcc gaggtgacgg 600
 gcatgagctt cctcgcctgc gatgtcggcg tgagcgcccg aaataagcgt aagcacgcgg 660
 cggcgcagtt gtactcgcgc ccgccgagcc cgagcggcgt gatcggcgcg ctgtcctgct 720
 tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcggc ccgtgggcgc 780
 cgtcggcgct cgtgtccgtg tcgtcctctc cagagccacc aggtcggggc cccaagcgcg 840
 cagcggcggc gtcggcgctg gcgtcggcgt cagccggggc cgcgccaccg gtccagggtcc 900
 cgcacagct acccccccgc gaggagagcc gcgacgcctg gccgtccacc tgcgccgcgt 960
 gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcggtggc ggtggagaat 1020
 ggagaacaag gagcatcatt ggctcgcgct ggtgagcagg agaacgaact attttgccca 1080
 ttgccgtgac agatgggggg tggtcactgc gtggagccgc gctgancaat ga 1132

<210> 24
 <211> 318
 <212> PRT
 <213> Zea mays

<400> 24
 Asn Ser Ala Arg Ala Ala Val Gly Trp Val Ser Arg Ala Ala Ala Arg
 1 5 10 15
 Leu Gly Phe Ser Ala Leu Thr Ala Ala Leu Ala Ala Tyr Leu Asp
 20 25 30
 Arg Cys Phe Leu Pro Gly Gly Ala Leu Arg Leu Gly Asp Gln Pro Trp
 35 40 45
 Met Ala Arg Leu Ala Ala Val Thr Cys Phe Ala Leu Ala Ala Lys Val
 50 55 60
 Glu Glu Thr Arg Val Pro Pro Leu Leu Asp Leu Gln Leu Tyr Ala Ala
 65 70 75 80
 Ala Asp Ala Ala Asp Pro Tyr Val Phe Glu Ala Lys Thr Val Arg Arg
 85 90 95
 Met Glu Leu Leu Val Leu Ser Ala Leu Gly Trp Arg Met His Pro Val
 100 105 110
 Thr Pro Phe Ser Tyr Leu Gln Pro Val Leu Ala Asp Ala Ala Thr Arg
 115 120 125
 Leu Arg Ser Cys Glu Gly Val Leu Leu Ala Val Met Ala Asp Trp Arg
 130 135 140
 Trp Pro Arg His Arg Pro Ser Ala Trp Ala Ala Ala Leu Leu Ile
 145 150 155 160
 Thr Ala Ala Ala Gly Asp Gly Gly Asp Gly Asp Gly Asp Thr Glu Leu
 165 170 175

Leu Ala Leu Ile Asn Ala Pro Glu Asp Lys Thr Ala Glu Cys Ala Lys
 180 185 190
 Ile Ile Ser Glu Val Thr Gly Met Ser Phe Leu Ala Cys Asp Val Gly
 195 200 205
 Val Ser Ala Gly Asn Lys Arg Lys His Ala Ala Ala Gln Leu Tyr Ser
 210 215 220
 Pro Pro Pro Ser Pro Ser Gly Val Ile Gly Ala Leu Ser Cys Phe Ser
 225 230 235 240
 Cys Glu Ser Ser Thr Ser Ala Thr Ala Met Ala Ala Ala Val Gly Pro
 245 250 255
 Trp Ala Pro Ser Ala Ser Val Ser Val Ser Ser Ser Pro Glu Pro Pro
 260 265 270
 Gly Arg Ala Pro Lys Arg Ala Ala Ala Ala Ser Ala Ser Ala Ser Ala
 275 280 285
 Ser Ala Gly Val Ala Pro Pro Val Gln Val Pro His Gln Leu Pro Pro
 290 295 300
 Asp Glu Glu Ser Arg Asp Ala Trp Pro Ser Thr Cys Ala Ala
 305 310 315

<210> 25
 <211> 674
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (527)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (561)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (640)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (643)
 <223> n = A, C, G or T

<400> 25
 cactcactca ccccttcctt tctaactcct caaattgtgt gttctgagaa tggaaatgcc 60
 tccttctcca tcgggggcatt ccgcactctc catcccataa aagtcccaga tccaagatgg 120
 cttaccacca tcaaaaatcc cttttggaca ccctatactg ctccgaagag cattggatag 180
 gggaagggtga atttgaccaa gcagaggagg agtacggtaa cagtaatagc aatagtagca 240
 gcaccttagt aaacaactcc cctgagtcct cccctcattt gttgctcgaa agcgacatgt 300
 tttgggacga acaagagttg gcatcgctgt tggagaaaga acaacacaac ccactaagca 360
 cttgctgtct ccaaagcaac cctgccttgg aggggtgctcg catagaagcc gtggagtgga 420
 ttctcaaagt aaacgcccac tactccttct ctgccctcac cgctgttctt gctgtcaact 480
 actttgaccg ttttctcttc agcttccgct ttcagaatga cattaancca tggatgactc 540
 ggggtcgctg ccgtcgcttg nctctccctc gctgccaaag tgggcgagac acacgttccc 600
 tttcttattt gacccttcaa caaagtggga ggaggagtan atnctttgtt ccaagccaaa 660
 gacgattaaa aaag 674

<210> 26
 <211> 186
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (137)
 <223> Xaa = ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (149)
 <223> Xaa = ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (175)..(176)
 <223> Xaa = ANY AMINO ACID

<400> 26
 Met Ala Tyr His His Gln Lys Ser Leu Leu Asp Thr Leu Tyr Cys Ser
 1 5 10 15
 Glu Glu His Trp Ile Gly Glu Gly Glu Phe Asp Gln Ala Glu Glu Glu
 20 25 30
 Tyr Gly Asn Ser Asn Ser Asn Ser Ser Thr Leu Val Asn Asn Ser
 35 40 45
 Pro Glu Ser Ser Pro His Leu Leu Leu Glu Ser Asp Met Phe Trp Asp
 50 55 60
 Glu Gln Glu Leu Ala Ser Leu Leu Glu Lys Glu Gln His Asn Pro Leu
 65 70 75 80
 Ser Thr Cys Cys Leu Gln Ser Asn Pro Ala Leu Glu Gly Ala Arg Ile
 85 90 95
 Glu Ala Val Glu Trp Ile Leu Lys Val Asn Ala His Tyr Ser Phe Ser
 100 105 110
 Ala Leu Thr Ala Val Leu Ala Val Asn Tyr Phe Asp Arg Phe Leu Phe
 115 120 125
 Ser Phe Arg Phe Gln Asn Asp Ile Xaa Pro Trp Met Thr Arg Gly Arg
 130 135 140
 Cys Arg Arg Leu Xaa Leu Pro Arg Cys Gln Ser Gly Arg Asp Thr Arg
 145 150 155 160
 Ser Leu Ser Tyr Leu Thr Leu Gln Gln Ser Gly Arg Arg Ser Xaa Xaa
 165 170 175
 Phe Val Pro Ser Gln Arg Arg Leu Lys Lys
 180 185

<210> 27
 <211> 554
 <212> DNA
 <213> Glycine max

<400> 27
 ctccttttca ccttttcttca tagcctacca cttttctgct ttcattctact ctcacttctc 60
 ttcacacact gagacacaca gagagagaaa aataaagggt gtgatgggtg tcttactgag 120

```

tggttttcttt ttataatgaa caaagaactg cacaccctct tcttcaccga agaagaagat 180
ggcaattcag caccacaatg accaactaga gcataatgaa aatgtctcat ctgtccttga 240
tgcccttttac tgtgacgaag gaaagtggga agaggaagag gaggagaaag aagaagaaga 300
agatgaaggt gaaaatgaaa gtgaagtgaac aacaaacact gcaacttgtc ttttccctct 360
gctcttggtg gagcaagact tgttctggga agatgaggaa ctaaactcta tcttttccaa 420
agagaagggt caacatgaag aagcctatgg tataacaatc tgaacagtga tgtgtataac 480
aacaacaaca atactagtat ataatgtgat ttggctcttg ctcttcagct cgtcggagcg 540
tgatgatgct gaat 554

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<210> 28
<211> 94
<212> PRT
<213> Glycine max

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<400> 28
Met Ala Ile Gln His His Asn Asp Gln Leu Glu His Asn Glu Asn Val
1 5 10 15
Ser Ser Val Leu Asp Ala Leu Tyr Cys Asp Glu Gly Lys Trp Glu Glu
20 25 30
Glu Glu Glu Glu Lys Glu Glu Glu Asp Glu Gly Glu Asn Glu Ser
35 40 45
Glu Val Thr Thr Asn Thr Ala Thr Cys Leu Phe Pro Leu Leu Leu Leu
50 55 60
Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Asn Ser Ile Phe Ser
65 70 75 80
Lys Glu Lys Val Gln His Glu Glu Ala Tyr Gly Ile Thr Ile
85 90

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<210> 29
<211> 372
<212> PRT
<213> Catharanthus roseus

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<400> 29
Met Ala Asp Lys Glu Asn Cys Ile Arg Val Thr Arg Leu Ala Lys Lys
1 5 10 15
Arg Ala Val Glu Ala Met Ala Ala Ser Glu Gln Gln Arg Pro Ser Lys
20 25 30
Lys Arg Val Val Leu Gly Glu Leu Lys Asn Leu Ser Ser Asn Ile Ser
35 40 45
Ser Ile Gln Thr Tyr Asp Phe Ser Ser Gly Pro Gln Lys Gln Gln Lys
50 55 60
Asn Lys Asn Lys Arg Lys Ala Lys Glu Ser Leu Gly Phe Glu Val Lys
65 70 75 80
Glu Lys Lys Val Glu Glu Ala Gly Ile Asp Val Phe Ser Gln Ser Asp
85 90 95
Asp Pro Gln Met Cys Gly Ala Tyr Val Ser Asp Ile Tyr Glu Tyr Leu
100 105 110
His Lys Met Glu Met Glu Thr Lys Arg Arg Pro Leu Pro Asp Tyr Leu
115 120 125
Asp Lys Val Gln Lys Asp Val Thr Ala Asn Met Arg Gly Val Leu Ile
130 135 140

```

Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Leu Pro Asp Thr
 145 150 155 160
 Leu Tyr Leu Thr Val Ser Tyr Ile Asp Arg Phe Leu Ser Met Asn Ala
 165 170 175
 Leu Ser Arg Gln Lys Leu Gln Leu Leu Gly Val Ser Ser Met Leu Ile
 180 185 190
 Ala Ser Lys Tyr Glu Glu Ile Ser Pro Pro His Val Glu Asp Phe Cys
 195 200 205
 Tyr Ile Thr Asp Asn Thr Tyr Lys Lys Glu Glu Val Val Lys Met Glu
 210 215 220
 Ala Asp Val Leu Lys Phe Leu Lys Phe Glu Met Gly Asn Pro Thr Ile
 225 230 235 240
 Lys Thr Phe Leu Arg Arg Leu Thr Arg Val Val Gln Asp Gly Asp Lys
 245 250 255
 Asn Pro Asn Leu Gln Phe Glu Phe Leu Gly Tyr Tyr Leu Ala Glu Leu
 260 265 270
 Ser Leu Leu Asp Tyr Gly Cys Val Lys Phe Leu Pro Ser Leu Ile Ala
 275 280 285
 Ser Ser Val Ile Phe Leu Ser Arg Phe Thr Leu Gln Pro Lys Val His
 290 295 300
 Pro Trp Asn Ser Leu Leu Gln His Asn Ser Gly Tyr Lys Pro Ala Asp
 305 310 315 320
 Leu Lys Glu Cys Val Leu Ile Ile His Asp Leu Gln Leu Ser Lys Arg
 325 330 335
 Gly Ser Ser Leu Val Ala Val Arg Asp Lys Tyr Lys Gln His Lys Phe
 340 345 350
 Lys Cys Val Ser Thr Leu Thr Ala Pro Pro Ser Ile Pro Asp Glu Phe
 355 360 365
 Phe Glu Asp Ile
 370
 <210> 30
 <211> 335
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 30
 Met Arg Ser Tyr Arg Phe Ser Asp Tyr Leu His Met Ser Val Ser Phe
 1 5 10 15
 Ser Asn Asp Met Asp Leu Phe Cys Gly Glu Asp Ser Gly Val Phe Ser
 20 25 30
 Gly Glu Ser Thr Val Asp Phe Ser Ser Ser Glu Val Asp Ser Trp Pro
 35 40 45
 Gly Asp Ser Ile Ala Cys Phe Ile Glu Asp Glu Arg His Phe Val Pro
 50 55 60
 Gly His Asp Tyr Leu Ser Arg Phe Gln Thr Arg Ser Leu Asp Ala Ser
 65 70 75 80

Cys Leu Ser Phe Met Val Gln Arg Glu Met Glu Phe Leu Pro Lys Asp
 65 70 75 80
 Asp Tyr Val Glu Arg Leu Arg Ser Gly Asp Leu Asp Leu Ser Val Arg
 85 90 95
 Lys Glu Ala Leu Asp Trp Ile Leu Lys Ala His Met His Tyr Gly Phe
 100 105 110
 Gly Glu Leu Ser Phe Cys Leu Ser Ile Asn Tyr Leu Asp Arg Phe Leu
 115 120 125
 Ser Leu Tyr Glu Leu Pro Arg Ser Lys Thr Trp Thr Val Gln Leu Leu
 130 135 140
 Ala Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Ile Asn Val
 145 150 155 160
 Pro Leu Thr Val Asp Leu Gln Val Gly Asp Pro Lys Phe Val Phe Glu
 165 170 175
 Gly Lys Thr Ile Gln Arg Met Glu Leu Leu Val Leu Ser Thr Leu Lys
 180 185 190
 Trp Arg Met Gln Ala Tyr Thr Pro Tyr Thr Phe Ile Asp Tyr Phe Met
 195 200 205
 Arg Lys Met Asn Gly Asp Gln Ile Pro Ser Arg Pro Leu Ile Ser Gly
 210 215 220
 Ser Met Gln Leu Ile Leu Ser Ile Ile Arg Ser Ile Asp Phe Leu Glu
 225 230 235 240
 Phe Arg Ser Ser Glu Ile Ala Ala Ser Val Ala Met Ser Val Ser Gly
 245 250 255
 Glu Ile Gln Ala Lys Asp Ile Asp Lys Ala Met Pro Cys Phe Phe Ile
 260 265 270
 His Leu Asp Lys Gly Arg Val Gln Lys Cys Val Glu Leu Ile Gln Asp
 275 280 285
 Leu Thr Thr Ala Thr Ile Thr Thr Ala Ala Ala Ala Ser Leu Val Pro
 290 295 300
 Gln Ser Pro Ile Gly Val Leu Glu Ala Ala Ala Cys Leu Ser Tyr Lys
 305 310 315 320
 Ser Gly Asp Glu Arg Thr Val Gly Ser Cys Thr Thr Ser Ser His Thr
 325 330 335
 Lys Arg Arg Lys Leu Asp Thr Ser Ser Leu Glu His Gly Thr Ser Glu
 340 345 350

Lys Leu

<210> 32
 <211> 373
 <212> PRT
 <213> Nicotiana tabacum

<400> 32
 Met Ala Ile Glu His Asn Glu Gln Gln Glu Leu Ser Gln Ser Phe Leu
 1 5 10 15

Leu	Asp	Ala	Leu	Tyr	Cys	Glu	Glu	Glu	Glu	Glu	Lys	Trp	Gly	Asp	Leu	20	25	30
Val	Asp	Asp	Glu	Thr	Ile	Ile	Thr	Pro	Leu	Ser	Ser	Glu	Val	Thr	Thr	35	40	45
Thr	Thr	Thr	Thr	Thr	Thr	Lys	Pro	Asn	Ser	Leu	Leu	Pro	Leu	Leu	Leu	50	55	60
Leu	Glu	Gln	Asp	Leu	Phe	Trp	Glu	Asp	Glu	Glu	Leu	Leu	Ser	Leu	Phe	65	70	75
Ser	Lys	Glu	Lys	Glu	Thr	His	Cys	Trp	Phe	Asn	Ser	Phe	Gln	Asp	Asp	85	90	95
Ser	Leu	Leu	Cys	Ser	Ala	Arg	Val	Asp	Ser	Val	Glu	Trp	Ile	Leu	Lys	100	105	110
Val	Asn	Gly	Tyr	Tyr	Gly	Phe	Ser	Ala	Leu	Thr	Ala	Val	Leu	Ala	Ile	115	120	125
Asn	Tyr	Phe	Asp	Arg	Phe	Leu	Thr	Ser	Leu	His	Tyr	Gln	Lys	Asp	Lys	130	135	140
Pro	Trp	Met	Ile	Gln	Leu	Ala	Ala	Val	Thr	Cys	Leu	Ser	Leu	Ala	Ala	145	150	155
Lys	Val	Glu	Glu	Thr	Gln	Val	Pro	Leu	Leu	Leu	Asp	Phe	Gln	Val	Glu	165	170	175
Asp	Ala	Lys	Tyr	Val	Phe	Glu	Ala	Lys	Thr	Ile	Gln	Arg	Met	Glu	Leu	180	185	190
Leu	Val	Leu	Ser	Ser	Leu	Lys	Trp	Arg	Met	Asn	Pro	Val	Thr	Pro	Leu	195	200	205
Ser	Phe	Leu	Asp	His	Ile	Ile	Arg	Arg	Leu	Gly	Leu	Arg	Asn	Asn	Ile	210	215	220
His	Trp	Glu	Phe	Leu	Arg	Arg	Cys	Glu	Asn	Leu	Leu	Leu	Ser	Ile	Met	225	230	235
Ala	Asp	Cys	Arg	Phe	Val	Arg	Tyr	Met	Pro	Ser	Val	Leu	Ala	Thr	Ala	245	250	255
Ile	Met	Leu	His	Val	Ile	His	Gln	Val	Glu	Pro	Cys	Asn	Ser	Val	Asp	260	265	270
Tyr	Gln	Asn	Gln	Leu	Leu	Gly	Val	Leu	Lys	Ile	Asn	Lys	Glu	Lys	Val	275	280	285
Asn	Asn	Cys	Phe	Glu	Leu	Ile	Ser	Glu	Val	Cys	Ser	Lys	Pro	Ile	Ser	290	295	300
His	Lys	Arg	Lys	Tyr	Glu	Asn	Pro	Ser	His	Ser	Pro	Ser	Gly	Val	Ile	305	310	315
Asp	Pro	Ile	Tyr	Ser	Ser	Glu	Ser	Ser	Asn	Asp	Ser	Trp	Asp	Leu	Glu	325	330	335
Ser	Thr	Ser	Ser	Tyr	Phe	Pro	Val	Phe	Lys	Lys	Ser	Arg	Val	Gln	Glu	340	345	350
Gln	Gln	Met	Lys	Leu	Ala	Ser	Ser	Ile	Ser	Arg	Val	Phe	Val	Glu	Ala	355	360	365

Val Gly Ser Pro His
370